

SCORE Search Results Details for Application 10597173 and Search Result 20070521_150829_us-10-597-173b-7.100align.rge.

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GenCore version 6.2.1
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DM nucleic - nucleic search, using sw model

Run on: May 23, 2007, 00:36:17 ; Search time 817 Seconds
(without alignments)
1268.619 Million cell updates/sec

Title: US-10-597-173B-7

Perfect score: 15

Sequence: 1 ttctttgaaaaactga 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : GenEmbl:
1: gb_env:
2: gb_pat:
3: gb_ph:
4: gb_pl:
5: gb_pr:
6: gb_ro:
7: gb_sts:
8: gb_sy:

RESULT 44

JRED6PCA

LOCUS URED6PCA 305 bp DNA linear BCT 21-MAY-1995
 DEFINITION *Ureaplasma canigenitalium* (canine ureaplasma) 16S-23S rRNA genes, intergenic spacer region.
 ACCESSION D63684
 VERSION D63684.1 GI:944983
 KEYWORDS 16S rRNA; 23S rRNA.
 SOURCE *Ureaplasma canigenitalium*
 ORGANISM *Ureaplasma canigenitalium*
 Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; *Ureaplasma*.
 REFERENCE 1
 AUTHORS Harasawa, R., Lefkowitz, E.J., Glass, J.I. and Cassell, G.H.
 TITLE Phylogenetic analysis of the 16S-23S rRNA intergenic spacer regions of the genus *Ureaplasma*
 JOURNAL J. Vet. Med. Sci. 58 (3), 191-195 (1996)
 PUBMED 8777224
 REFERENCE 2 (bases 1 to 305)
 AUTHORS Harasawa, R.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUL-1995) Ryo Harasawa, The University of Tokyo Faculty of Medicine, Animal Center for Biomdeical Research; Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:ryo@m.u-tokyo.ac.jp, Tel:+81-3-5841-3623, Fax:+81-3-5841-3679)
 FEATURES Location/Qualifiers
 source 1. .305
 /organism="Ureaplasma canigenitalium"
 /mol_type="genomic DNA"
 /strain="D6P-C"
 /specific_host="canine"
 /db_xref="taxon:42092"
 misc_feature 1. .305
 /note="16S-23S rRNA genes intergenic spacer region"

ORIGIN

Query Match 100.0%; Score 15; DB 15; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCTTTGAAACTGA 15
 |||||||
 Db 180 TTCTTTGAAACTGA 194

RESULT 45

AJ780992

LOCUS AJ780992 305 bp DNA linear BCT 28-JUL-2004
 DEFINITION *Mycoplasma gallinarum* 16S-23S intergenic spacer, type strain PG16T.